Multimodal human brain mapping in a new analysis and visualization software environment

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1 Introduction

During the last years, interest has grown in novel methods for mapping human brain function. The relevant techniques are functional magnetic resonance imaging (fMRI), magnetoencephalography (MEG). The comparison of those different techniques can be performed by multimodal mapping to test the validity of the different modalities in one analysis environment. Moreover, multimodal mapping increases the reliability in the results of a single modality.

In the work presented here, a new software platform – Open Magnetic and Electric Graphic Analysis (OMEGA) [1] – has been developed that includes the analysis of fMRI image series, tools for volume modeling of MRI data and the localization of functional human brain areas by solving the inverse problem for MEG data sets. The fast tools and algorithms enable a complete and user-independent analysis to compare and integrate the localization results of brain mapping with co-registered different modalities:

- fMRI analysis and visualization of the results
- volume modeling of morphological MRI data and generate multi-compartment models
- MEG analysis and source localization using multi-compartment models in solving the inverse problem. Sources can be modeled by localized single or multiple dipoles as well as by distributed currents. Anatomical constraints for the source space can be included, too
- visualization of the localization results of the different modalities on the morphological background

The OMEGA software has been developed under a multi-platform environment and therefore can run on workstation (UNIX) as well as on PC (Linux) and can take advantage of multiprocessor systems.

2 Methods

2.1 Functional magnetic resonance imaging

The fMRI-part of OMEGA consists of several modules [2] including visualization, motion correction and functional analysis:

2.1.1 Visualization

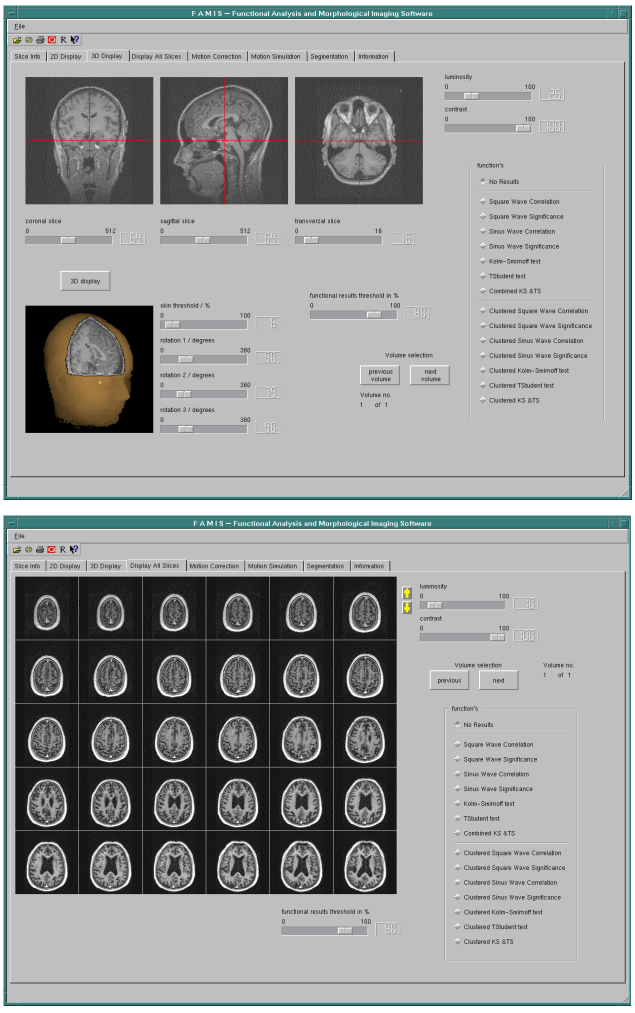


Figure 1: *3D representation (upper image) and stamp representation (lower image) of morphological MRI-data.*

The visualization module for the morphologic MRI data sets is easy to handle for the user and shows the morphologic data in two(2D)- and three(3D)-dimensional form (Fig. 1).

2.1.2 Motion correction

A module for the motion correction of fMRI data is used to correct brain movements that are caused by shifting as well as by rotations. General experiences show that it is a good practice to use the motion correction as a prerequisite for the functional analysis. The motion correction is performed under the following assumptions:

- the brain is considered as a rigid body that can move slightly with 6 degrees of freedom
- there are no relative movements of single parts. The brain is not pulsating.
- the central slice of the 3D MRI data set acts as a reference slice with its contour acting as the reference for the motion correction

The rotation and shifting matrices R and T are determined:

$$\vec{x}^{(2)} = \Rightarrow{R}\,\vec{x}^{(1)} + \Rightarrow{T}$$

where $x^{(1)}$ and $x^{(2)}$ are the position vectors of voxels of slice 1 or 2, respectively. These matrices minimize the error between two central slices of subsequent recorded 3D volumes. The minimization can be performed either by Levenberg-Marquardt-method or by Conjugated-Simplex-method.

The resulting matrix is used for the transformation of the whole 3D data set. Thus, the motion correction is automatically performed and no interference of the operator is required.

About 2 seconds are needed to calculate the motion correction for a 3D-volume consisting of 16 slices (128x128 pixel) on a high end hardware equipment, i.e. dual processor Pentium III PC, 800 MHz.

2.1.3 Functional analysis

Several deterministic analysis tools and several statistical analysis tools (for a detailed description of the algorithms see [3]) are included to detect the brain activation from the functional analysis of the motion corrected fMRI-data.

To improve the signal to noise ratio, averaging of fMRI data sets is performed over voxels which are assumed to belong to the same functional. The groups of voxels to be averaged are defined by a hierarchical clustering procedure. The similarity of the voxels is defined on the basis of several properties:

- intensity of stimulus correlated signals
- correlation of the time course of the voxels
- geometrical distance (near voxels are more likely to belong to the same structure)

After clustering, a threshold is set to identify the groups of voxels to be averaged and the spatial average is performed. After averaging, the amplitude of the signal of each voxel in phase with the stimulus on/off function is calculated.

The regions received from the functional analysis can be integrated in the morphology. They are color coded areas displayed on the background of the corresponding morphologic MRI images (Figs. 2 and 3).

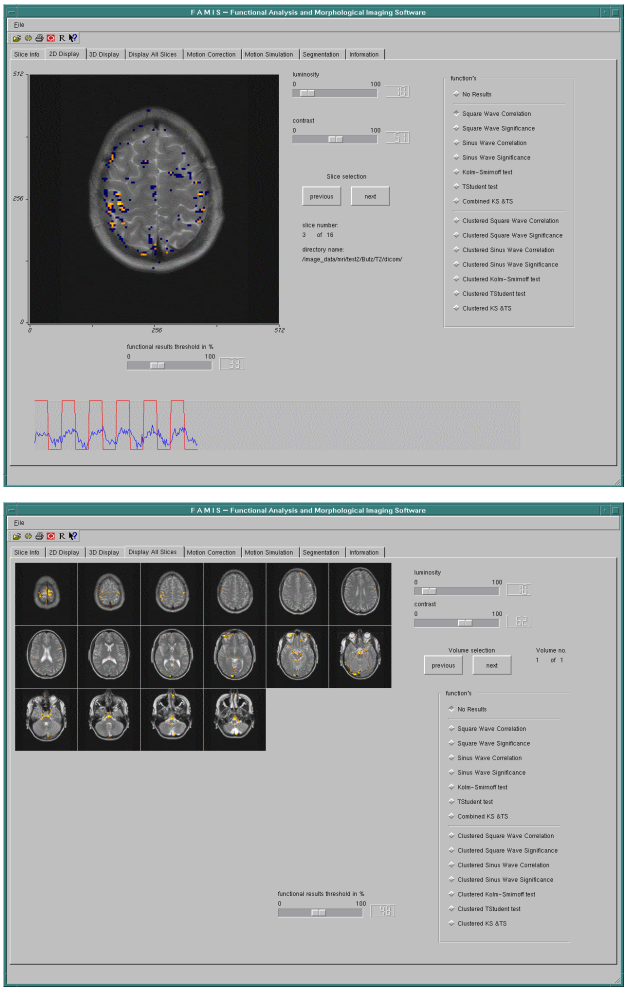


Figure 2**:** *Functional results.*

For data sets with less than 100 volumes the standard functional analysis is performed within some 10 seconds. The signal to noise ratio improvement with cluster analysis is performed below 1 minute for a set of volumes, each consisting of 16 slices (128x128 pixel) on the hardware equipment mentioned above, of course depending on the analysis method.

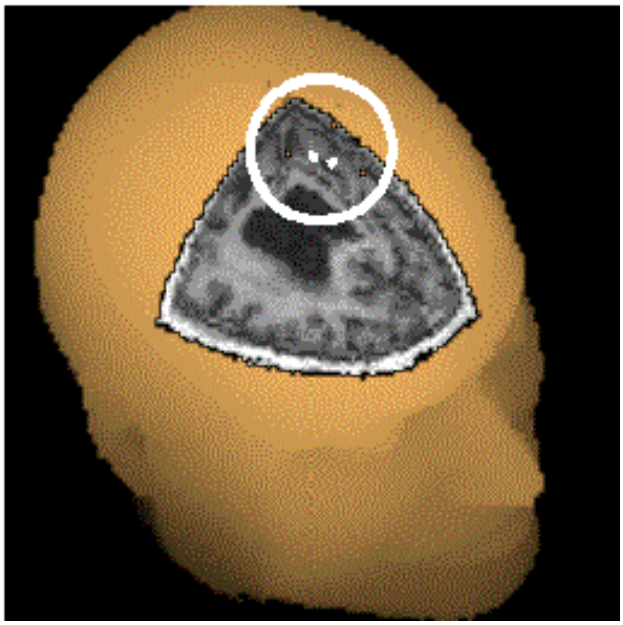
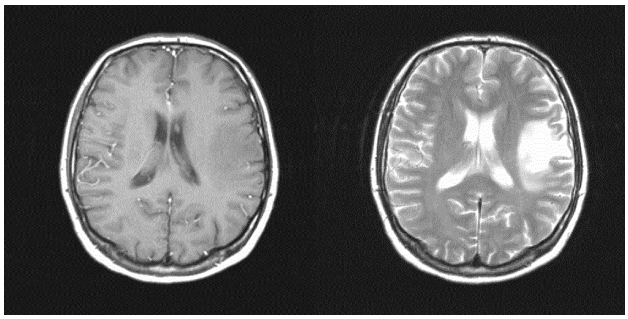


Figure 3: *Functional results integrated to the whole head recording. For a better visualization, the significant areas are highlighted*

2.2 Volume modeling

The segmentation of three shells is performed automatically from morphological MRI data sets. The basis of this segmentation is an automatically threshold finding. The three segmented shells are the outer skull, the inner bone and the gray matter of the brain.



(a) (b)

Figure 4**:** *Examples for T1(a)- and T2(b)-weighted images.*

For T_1- or T_2-weighted images we use different techniques for extracting the gray matter. As it can be seen from Fig. 4 the T_1 weighted images display no white matter. Therefore, to extract the gray matter from T_1 weighted data sets the automatic detection of a lower threshold is sufficient, whereas for T_2 weighted images, an upper and a lower threshold have to be applied for finding the voxels that belong to the brain.

Those segmented shells are triangulated with 200 up to 1800 vertex points. The triangulation procedure is based on a blowing-up-technique. This technique first generates a triangulated sphere in the center of the segmented shell. Then, the sphere is blown up till it reaches the segmented shell.
The whole segmentation and triangulation procedure is performed within 10 seconds for a morphological volume, consisting of 40 slices (256x256 pixel). Fig. 5 shows the triangulated surface of the skin of a whole head.

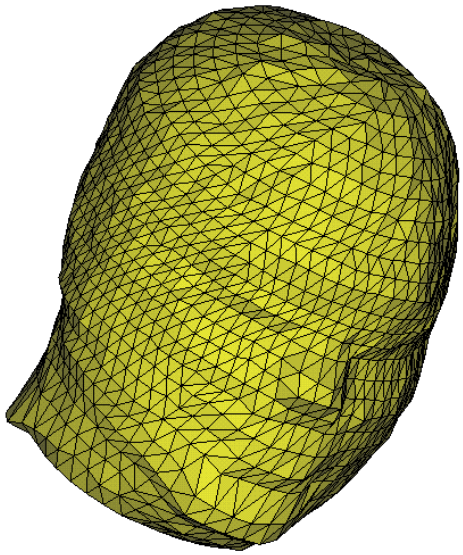


Figure 5**:** *Segmented and triangulated whole head.*

2.3 Magnetoencephalography

In numerical modeling of biomagnetic fields in the human brain, the basic goal is not only to show the anatomical structure but also to present calculated electromagnetic fields and localized sources in the morphological environment.
OMEGA provides the possibility to present calculated fields, i.e. the electromagnetic information, in combination with the anatomy. The working scene for the presentation of the electromagnetic fields and the anatomical objects is a rotating 3D-cube controlled by so called virtual trackball which enables the rotation in any direction. The scalar fields can be displayed in a form of isocontours or equifilled regions and the vector fields can be shown as a set of solid cones.
Common dipole reconstruction methods are normally applied with non-linear least-squares parameter estimations for solving the inverse problems. These methods need costly computation

time if instead of an analytical volume conductor (sphere, halfspace, ellipsoid, etc.) realistic geometry models are involved.
In the OMEGA software a linear iterative algorithm for dipole localization is implemented. This algorithm provides the possibility of computing dipole localization in analytically described surfaces as well as in realistic triangulated surfaces in a time which is in a useful range for routine applications of biomagnetism [4].
The goal in solving of the biomagnetic inverse problems, is to calculate the source current density distributions producing the magnetic signals measured outside the body. The method that is implemented in OMEGA to realize this task is based on the minimum-norm approach [5]. Weighting matrices to eliminate depth bias of localized sources and to correct the lead field matrix [6] are used. The Tikhonov-like regularization [7] is used in the process of solution for balancing noise influence. The source space where the current distribution is reconstructed can be defined as a regular 3D grid of current dipoles locations or it can be described as a 2D surface arising from physiological constrains.

3 Discussion

Multimodal imaging is a prerequisite to test the clinical validation of different techniques to map activated human brain areas. In this work we have presented a software platform that performs this task on workstation as well as on PC. For clinical applicability, the requests on an analysis software performing multimodal brain imaging are that it is fast and restricted to the minimal interference of the user. The software environment OMEGA we presented here is designed and developed to fulfil these requests in clinical applications.

References

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